

SEQUENCE LISTING

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<120> NOVEL OXIDASE

<130> Q83855

<150> PCT/JP03/07148

<151> 2003-06-05

<150> JP 2002-165612

<151> 2002-06-06

<150> JP 2002-060749

<151> 2003-03-07

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<170> PatentIn version 3.1

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gtt tgg tta ggg ctg aat gtt ttc ctg ttt gtg gat gcc ttc ctg aaa	96
Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Asp Ala Phe Leu Lys	
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tat gag aag gcc gac aaa tac tac tac aca aga aaa atc ctt ggg tca	144
Tyr Glu Lys Ala Asp Lys Tyr Tyr Tyr Thr Arg Lys Ile Leu Gly Ser	
35 40 45	

aca ttg gcc tgt gcc cga gcg tct gct ctc tgc ttg aat ttt aac agc	192
Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe Asn Ser	
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acg ctg atc ctg ctt cct gtg tgt cgc aat ctg ctg tcc ttc ctg agg	240
Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser Phe Leu Arg	
65 70 75 80	

ggc acc tgc tca ttt tgc agc cgc aca ctg aga aag caa ttg gat cac	288
Gly Thr Cys Ser Phe Cys Ser Arg Thr Leu Arg Lys Gln Leu Asp His	
85 90 95	

aac ctc acc ttc cac aag ctg gtg gcc tat atg atc tgc cta cat aca	336
Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys Leu His Thr	
100 105 110	

gct att cac atc att gca cac ctg ttt aac ttt gac tgc tat agc aga Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Asp Cys Tyr Ser Arg 115 120 125	384
agc cga cag gcc aca gat ggc tcc ctt gcc tcc att ctc tcc agc cta Ser Arg Gln Ala Thr Asp Gly Ser Leu Ala Ser Ile Leu Ser Ser Leu 130 135 140	432
tct cat gat gag aaa aag ggg ggt tct tgg cta aat ccc atc cag tcc Ser His Asp Glu Lys Lys Gly Gly Ser Trp Leu Asn Pro Ile Gln Ser 145 150 155 160	480
cga aac acg aca gtg gag tat gtg aca ttc acc agc gtt gct ggt ctc Arg Asn Thr Thr Val Glu Tyr Val Thr Phe Thr Ser Val Ala Gly Leu 165 170 175	528
act gga gtg atc atg aca ata gcc ttg att ctc atg gta act tca gct Thr Gly Val Ile Met Thr Ile Ala Leu Ile Leu Met Val Thr Ser Ala 180 185 190	576
act gag ttc atc cgg agg agt tat ttt gaa gtc ttc tgg tat act cac Thr Glu Phe Ile Arg Arg Ser Tyr Phe Glu Val Phe Trp Tyr Thr His 195 200 205	624
cac ctt ttt atc ttc tat atc ctt ggc tta ggg att cac ggc att ggt His Leu Phe Ile Phe Tyr Ile Leu Gly Leu Gly Ile His Gly Ile Gly 210 215 220	672
gga att gtc cgg ggt caa aca gag gag agc atg aat gag agt cat cct Gly Ile Val Arg Gly Gln Thr Glu Glu Ser Met Asn Glu Ser His Pro 225 230 235 240	720
cgc aag tgt gca gag tct ttt gag atg tgg gat gat cgt gac tcc cac Arg Lys Cys Ala Glu Ser Phe Glu Met Trp Asp Asp Arg Asp Ser His 245 250 255	768
tgt agg cgc cct aag ttt gaa ggg cat ccc cct gag tct tgg aag tgg Cys Arg Arg Pro Lys Phe Glu Gly His Pro Pro Glu Ser Trp Lys Trp 260 265 270	816
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tac cgc tcc cag cag aag gtt gtg att acc aag gtt gtt atg cac cca Tyr Arg Ser Gln Gln Lys Val Val Ile Thr Lys Val Val Met His Pro 290 295 300	912
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 370 375 380

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 Val Gly Ala Gly Ile Gly Val Thr Pro Phe Ala Ser Ile Leu Lys Ser
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atc tgg tac aaa ttc cag tgt gca gac cac aac ctc aaa aca aaa aag 1296
 Ile Trp Tyr Lys Phe Gln Cys Ala Asp His Asn Leu Lys Thr Lys Lys
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 Val Gly His Ala Ala Leu Asn Phe Asp Lys Ala Thr Asp Ile Val Thr
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 Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp Asp Asn Glu
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 Phe Ser Thr Ile Ala Thr Ser His Pro Lys Ser Val Val Gly Val Phe
 465 470 475 480

tta tgt ggc cct cgg act ttg gca aag agc ctg cgc aaa tgc tgt cac 1488
 Leu Cys Gly Pro Arg Thr Leu Ala Lys Ser Leu Arg Lys Cys Cys His
 485 490 495

cga tat tcc agt ctg gat cct aga aag gtt caa ttc tac ttc aac aaa 1536
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Tyr Glu Lys Ala Asp Lys Tyr Tyr Tyr Thr Arg Lys Ile Leu Gly Ser
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 Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser Phe Leu Arg
 65 70 75 80
 Gly Thr Cys Ser Phe Cys Ser Arg Thr Leu Arg Lys Gln Leu Asp His
 85 90 95
 Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys Leu His Thr
 100 105 110
 Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Asp Cys Tyr Ser Arg
 115 120 125
 Ser Arg Gln Ala Thr Asp Gly Ser Leu Ala Ser Ile Leu Ser Ser Leu
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 Ser His Asp Glu Lys Lys Gly Gly Ser Trp Leu Asn Pro Ile Gln Ser
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 Arg Asn Thr Thr Val Glu Tyr Val Thr Phe Thr Ser Val Ala Gly Leu
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 Thr Gly Val Ile Met Thr Ile Ala Leu Ile Leu Met Val Thr Ser Ala
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 Thr Glu Phe Ile Arg Arg Ser Tyr Phe Glu Val Phe Trp Tyr Thr His
 195 200 205
 His Leu Phe Ile Phe Tyr Ile Leu Gly Leu Gly Ile His Gly Ile Gly
 210 215 220
 Gly Ile Val Arg Gly Gln Thr Glu Glu Ser Met Asn Glu Ser His Pro
 225 230 235 240
 Arg Lys Cys Ala Glu Ser Phe Glu Met Trp Asp Asp Arg Asp Ser His
 245 250 255
 Cys Arg Arg Pro Lys Phe Glu Gly His Pro Pro Glu Ser Trp Lys Trp
 260 265 270

Ile Leu Ala Pro Val Ile Leu Tyr Ile Cys Glu Arg Ile Leu Arg Phe
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Tyr Arg Ser Gln Gln Lys Val Val Ile Thr Lys Val Val Met His Pro
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Ser Lys Val Leu Glu Leu Gln Met Asn Lys Arg Gly Phe Ser Met Glu
305 310 315 320

Val Gly Gln Tyr Ile Phe Val Asn Cys Pro Ser Ile Ser Leu Leu Glu
325 330 335

Trp His Pro Phe Thr Leu Thr Ser Ala Pro Glu Glu Asp Phe Phe Ser
340 345 350

Ile His Ile Arg Ala Ala Gly Asp Trp Thr Glu Asn Leu Ile Arg Ala
355 360 365

Phe Glu Gln Gln Tyr Ser Pro Ile Pro Arg Ile Glu Val Asp Gly Pro
370 375 380

Phe Gly Thr Ala Ser Glu Asp Val Phe Gln Tyr Glu Val Ala Val Leu
385 390 395 400

Val Gly Ala Gly Ile Gly Val Thr Pro Phe Ala Ser Ile Leu Lys Ser
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420 425 430

Val Gly His Ala Ala Leu Asn Phe Asp Lys Ala Thr Asp Ile Val Thr
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